

DT05 Rec'd PCT/PTO 03 FEB 2005

PG4912.seq.txt
SEQUENCE LISTING

<110> Glaxo Group Limited
Ellis, Jonathan H
Germaschewski, volker

<120> Antibodies

<130> SAL/PG4912

<140> unknown

<141> 2005-02-04

<150> PCT/EP03/08749

<151> 2003-07-17

<150> GB 0218230.1

<151> 2002-08-06

<150> GB 0218232.7

<151> 2002-08-06

<150> GB 0218234.3

<151> 2002-08-06

<150> GB 0218229.3

<151> 2002-08-06

<160> 32

<170> PatentIn version 3.1

<210> 1

<211> 17

<212> PRT

<213> Artificial sequence

<220>

<223> Light chain CDR

<400> 1

Lys Ser Ser His Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 2

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> Light chain CDR

<400> 2

Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Light chain CDR

<400> 3

His Gln Tyr Leu Ser Ser Leu Thr
1 5

<210> 4

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain CDR

<400> 4

Asn Tyr Gly Met Asn
1 5

<210> 5

<211> 17

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain CDR

<400> 5

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe Thr
1 5 10 15

Gly

<210> 6

<211> 17

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain CDR

<400> 6

Asn Pro Ile Asn Tyr Tyr Gly Ile Asn Tyr Glu Gly Tyr Val Met Asp
1 5 10 15

Tyr

<210> 7

<211> 51

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide encoding CDRL1

<400> 7

aagagcagcc acagcgtgct gtacagcagc aaccagaaga actacctggc c 51

<210> 8

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide encoding CDRL2

<400> 8

tgggccagca cccgcgagag c 21

<210> 9

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide encoding CDRL3

<400> 9

caccagtacc tgagcagcct gacc 24

<210> 10

<211> 15

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide encoding CDRH1

<400> 10

aactacggca tgaac

15

<210> 11

<211> 51

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide encoding CDRH2

<400> 11

tggatcaaca cctacaccgg cgagcccacc tacgccgacg acttcaccgg c

51

<210> 12

<211> 51

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide encoding CDRH3

<400> 12

aaccccatca actactacgg catcaactac gagggctacg tgatggacta c

51

<210> 13

<211> 126

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised antibody heavy chain variable region

<400> 13

Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asn Pro Ile Asn Tyr Tyr Gly Ile Asn Tyr Glu Gly Tyr Val
100 105 110

Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 14

<211> 126

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised antibody heavy chain variable region

<400> 14

Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

PG4912.seq.txt

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Asn Pro Ile Asn Tyr Tyr Gly Ile Asn Tyr Glu Gly Tyr Val
100 105 110

Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 15

<211> 126

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised antibody heavy chain variable region

<400> 15

Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

Ala Arg Asn Pro Ile Asn Tyr Tyr Gly Ile Asn Tyr Glu Gly Tyr Val
100 105 110

PG4912.seq.txt

Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 16

<211> 115

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised antibody light chain variable region

<400> 16

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser His Ser Val Leu Tyr Ser
 20 25 30

Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys His Gln
 85 90 95

Tyr Leu Ser Ser Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

Arg Thr Val
 115

<210> 17

<211> 115

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised antibody light chain variable region

<400> 17

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser His Ser Val Leu Tyr Ser
20 25 30

Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ile Asn Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys His Gln
85 90 95

Tyr Leu Ser Ser Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg Thr Val
115

<210> 18

<211> 115

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised antibody light chain variable region

<400> 18

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser His Ser Val Leu Tyr Ser
20 25 30

Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ser Ser Leu His Thr Glu Asp Val Ala Val Tyr Tyr Cys His Gln
 85 90 95

Tyr Leu Ser Ser Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

Arg Thr Val
 115

<210> 19

<211> 115

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised antibody light chain variable region

<400> 19

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser His Ser Val Leu Tyr Ser
 20 25 30

Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ile Asn Leu His Thr Glu Asp Val Ala Val Tyr Tyr Cys His Gln
 85 90 95

PG4912.seq.txt

Tyr Leu Ser Ser Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg Thr Val
115

<210> 20

<211> 378

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide sequence encoding the amino acid sequence SEQ ID N
0: 13

<400> 20
caggtgcagc tgggtgcaatc tgggtctgag ttgaagaagc ctggggcctc agtgaagggt 60
tcctgcaagg cttctggata caccttcact aactacggca tgaactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcaacacct acaccggcga gcccacctac 180
gccgacgact tcaccggccg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240
ctgcagatca gcagcctaaa ggctgaggac actgccgtgt attactgtgc gagaaacccc 300
atcaactact acggcatcaa ctacgagggc tacgtgatgg actactgggg ccagggcaca 360
ctagtcacag tctcctca 378

<210> 21

<211> 378

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide sequence encoding the amino acid sequence SEQ ID N
0: 14

<400> 21
caggtgcagc tgggtgcaatc tgggtctgag ttgaagaagc ctggggcctc agtgaagggt 60
tcctgcaagg cttctggata caccttcact aactacggca tgaactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcaacacct acaccggcga gcccacctac 180
gccgacgact tcaccggccg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

PG4912.seq.txt

| | |
|---|-----|
| ctgcagatca gcagcctaaa ggctgaggac actgccgtgt atttctgtgc gagaaacccc | 300 |
| atcaactact acggcatcaa ctacgagggc tacgtgatgg actactgggg ccagggcaca | 360 |
| ctagtcacag tctcctca | 378 |

<210> 22

<211> 378

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide sequence encoding the amino acid sequence SEQ ID N
O: 15

| | |
|--|-----|
| <400> 22 | |
| caggtgcagc tgggtgcaatc tgggtctgag ttgaagaagc ctggggcctc agtgaagggt | 60 |
| tcctgcaagg cttctggata caccttcact aactacggca tgaactgggt gcgacaggcc | 120 |
| cctggacaag ggcttgagtg gatgggatgg atcaacacct acaccggcga gcccacctac | 180 |
| gccgacgact tcaccggccg gtttgtcttc tccttgga cctctgtcag cacggcatat | 240 |
| ctgcagatca gcagcctaaa ggctgaggac actgccacct atttctgtgc gagaaacccc | 300 |
| atcaactact acggcatcaa ctacgagggc tacgtgatgg actactgggg ccagggcaca | 360 |
| ctagtcacag tctcctca | 378 |

<210> 23

<211> 345

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide sequence encoding the amino acid sequence SEQ ID N
O: 16

| | |
|---|-----|
| <400> 23 | |
| gacatcgtga tgaccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc | 60 |
| atcaactgca agagcagcca cagcgtgctg tacagcagca accagaagaa ctacctggcc | 120 |
| tgggtaccagc agaaaccagg acagcctcct aagctgctca ttactgggc atctacccgg | 180 |
| gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc | 240 |

atcagcagcc tgcaggctga agatgtggca gtttattact gtcaccagta cctgagcagc 300
 ctgacctttg gccaggggac caagctggag atcaaacgta cggtg 345

<210> 24

<211> 345

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide sequence encoding the amino acid sequence SEQ ID N
 O: 17

<400> 24
 gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60
 atcaactgca agagcagcca cagcgtgctg tacagcagca accagaagaa ctacctggcc 120
 tgggtaccagc agaaaccagg acagcctcct aagctgctca ttctactgggc atctaccg 180
 gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
 atcatcaacc tgcaggctga agatgtggca gtttattact gtcaccagta cctgagcagc 300
 ctgacctttg gccaggggac caagctggag atcaaacgta cggtg 345

<210> 25

<211> 345

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide sequence encoding the amino acid sequence SEQ ID N
 O: 18

<400> 25
 gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60
 atcaactgca agagcagcca cagcgtgctg tacagcagca accagaagaa ctacctggcc 120
 tgggtaccagc agaaaccagg acagcctcct aagctgctca ttctactgggc atctaccg 180
 gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
 atcagcagcc tgcacaccga agatgtggca gtttattact gtcaccagta cctgagcagc 300
 ctgacctttg gccaggggac caagctggag atcaaacgta cggtg 345

<210> 26

<211> 345

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide sequence encoding the amino acid sequence SEQ ID N
O: 19

```

<400> 26
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc      60
atcaactgca agagcagcca cagcgtgctg tacagcagca accagaagaa ctacctggcc      120
tggtaccagc agaaaccagg acagcctcct aagctgctca ttactgggc atctaccgg      180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc      240
atcatcaacc tgcacaccga agatgtggca gtttattact gtcaccagta cctgagcagc      300
ctgacctttg gccaggggac caagctggag atcaaacgta cggtg                        345

```

<210> 27

<211> 475

<212> PRT

<213> Artificial sequence

<220>

<223> Mouse/human chimeric anti-MAG antibody heavy chain

<400> 27

```

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1           5           10          15
Val His Ser Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
          20          25          30
Pro Gly Glu Thr Asn Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
          35          40          45
Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
          50          55          60
Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala
65          70          75          80

```

PG4912.seq.txt

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Asp | Asp | Phe | Thr | Gly 85 | Arg | Phe | Ala | Phe | Ser 90 | Leu | Glu | Thr | Ser | Ala 95 | Ser |
| Thr | Ala | Tyr | Leu 100 | Gln | Ile | Ser | Asn | Leu 105 | Lys | Asn | Glu | Asp | Thr 110 | Ala | Thr |
| Tyr | Phe | Cys 115 | Ala | Arg | Asn | Pro | Ile 120 | Asn | Tyr | Tyr | Gly | Ile 125 | Asn | Tyr | Glu |
| Gly | Tyr 130 | Val | Met | Asp | Tyr | Trp 135 | Gly | Gln | Gly | Thr | Leu 140 | Val | Thr | Val | Ser |
| Ser 145 | Ala | Ser | Thr | Lys | Gly 150 | Pro | Ser | Val | Phe | Pro 155 | Leu | Ala | Pro | Ser | Ser 160 |
| Lys | Ser | Thr | Ser | Gly 165 | Gly | Thr | Ala | Ala | Leu 170 | Gly | Cys | Leu | Val | Lys 175 | Asp |
| Tyr | Phe | Pro | Glu 180 | Pro | Val | Thr | Val | Ser 185 | Trp | Asn | Ser | Gly | Ala 190 | Leu | Thr |
| Ser | Gly | Val 195 | His | Thr | Phe | Pro | Ala 200 | Val | Leu | Gln | Ser | Ser 205 | Gly | Leu | Tyr |
| Ser | Leu 210 | Ser | Ser | Val | Val | Thr 215 | Val | Pro | Ser | Ser | Ser 220 | Leu | Gly | Thr | Gln |
| Thr 225 | Tyr | Ile | Cys | Asn | Val 230 | Asn | His | Lys | Pro | Ser 235 | Asn | Thr | Lys | Val | Asp 240 |
| Lys | Lys | Val | Glu | Pro 245 | Lys | Ser | Cys | Asp | Lys 250 | Thr | His | Thr | Cys | Pro 255 | Pro |
| Cys | Pro | Ala | Pro 260 | Glu | Leu | Ala | Gly | Ala 265 | Pro | Ser | Val | Phe | Leu 270 | Phe | Pro |
| Pro | Lys | Pro 275 | Lys | Asp | Thr | Leu | Met 280 | Ile | Ser | Arg | Thr | Pro 285 | Glu | Val | Thr |
| Cys | Val 290 | Val | Val | Asp | Val | Ser 295 | His | Glu | Asp | Pro | Glu 300 | Val | Lys | Phe | Asn |
| Trp 305 | Tyr | Val | Asp | Gly | Val 310 | Glu | Val | His | Asn | Ala 315 | Lys | Thr | Lys | Pro | Arg 320 |
| Glu | Glu | Gln | Tyr | Asn | Ser | Thr | Tyr | Arg | Val | Val | Ser | Val | Leu | Thr | Val |

325

335

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
340 345 350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
355 360 365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
370 375 380

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385 390 395 400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
405 410 415

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
420 425 430

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
435 440 445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
450 455 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 28

<211> 238

<212> PRT

<213> Artificial sequence

<220>

<223> Mouse/human chimeric anti-MAG antibody light chain

<400> 28

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala Val
20 25 30

PG4912.seq.txt

Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser His Ser Val
35 40 45

Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
50 55 60

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
65 70 75 80

Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

Thr Leu Thr Ile Ile Asn Val His Thr Glu Asp Leu Ala Val Tyr Tyr
100 105 110

Cys His Gln Tyr Leu Ser Ser Leu Thr Phe Gly Thr Gly Thr Lys Leu
115 120 125

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
130 135 140

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
195 200 205

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 29

<211> 475

<212> PRT

<213> Artificial sequence

<220>

<223> Mouse/human chimeric anti-MAG antibody heavy chain

<400> 29

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

Val His Ser Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
 20 25 30

Pro Gly Glu Thr Asn Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
 50 55 60

Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala
 65 70 75 80

Asp Asp Phe Thr Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
 85 90 95

Thr Ala Tyr Leu Gln Ile Ser Asn Leu Lys Asn Glu Asp Thr Ala Thr
 100 105 110

Tyr Phe Cys Ala Arg Asn Pro Ile Asn Tyr Tyr Gly Ile Asn Tyr Glu
 115 120 125

Gly Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 130 135 140

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
 145 150 155 160

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 165 170 175

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 180 185 190

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
 195 200 205

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
 210 215 220

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
 225 230 235 240

PG4912.seq.txt

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
 245 250 255
 Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 260 265 270
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 275 280 285
 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 290 295 300
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 305 310 315 320
 Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 325 330 335
 Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 340 345 350
 Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 355 360 365
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 370 375 380
 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 385 390 395 400
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 405 410 415
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 420 425 430
 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 435 440 445
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 450 455 460
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 465 470 475

<211> 475

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised anti-MAG antibody

<400> 30

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala
65 70 75 80

Asp Asp Phe Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser
85 90 95

Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Asn Pro Ile Asn Tyr Tyr Gly Ile Asn Tyr Glu
115 120 125

Gly Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
130 135 140

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
145 150 155 160

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
165 170 175

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
180 185 190

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
 195 200 205
 Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
 210 215 220
 Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
 225 230 235 240
 Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
 245 250 255
 Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
 260 265 270
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 275 280 285
 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 290 295 300
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 305 310 315 320
 Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 325 330 335
 Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 340 345 350
 Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 355 360 365
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 370 375 380
 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 385 390 395 400
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 405 410 415
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 420 425 430
 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 435 440 445

PG4912.seq.txt

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
450 455 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 31

<211> 238

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised anti-MAG antibody

<400> 31

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val
20 25 30

Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser His Ser Val
35 40 45

Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
50 55 60

Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
65 70 75 80

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr
100 105 110

Cys His Gln Tyr Leu Ser Ser Leu Thr Phe Gly Gln Gly Thr Lys Leu
115 120 125

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
130 135 140

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160

PG4912.seq.txt

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
195 200 205

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 32

<211> 475

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised anti-MAG antibody

<400> 32

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala
65 70 75 80

Asp Asp Phe Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser
85 90 95

Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val
Page 23

100

105

110

Tyr Tyr Cys Ala Arg Asn Pro Ile Asn Tyr Tyr Gly Ile Asn Tyr Glu
 115 120 125
 Gly Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 130 135 140
 Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
 145 150 155 160
 Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 165 170 175
 Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 180 185 190
 Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
 195 200 205
 Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
 210 215 220
 Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
 225 230 235 240
 Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
 245 250 255
 Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 260 265 270
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 275 280 285
 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 290 295 300
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 305 310 315 320
 Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 325 330 335
 Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 340 345 350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 355 360 365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 370 375 380

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 385 390 395 400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 405 410 415

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 420 425 430

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 435 440 445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 450 455 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 465 470 475